

**Figure 10:** Alignments of the genes proposed to be used in reassembly

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1                                     80
SEQ ID NO:114 (1)  ----AANLNGTLMQYFENYMPNDGQHWRKLQND SAYLA RHGITA VVI PPAYKCTS--QADVGYGAYDLYDLGEFFHQKGTVR
SEQ ID NO:128 (1)  -QANTAPVNGTMMQYFENDLPNDGTLWTKVKNKASSLSLGLTALMLPPAYKCTS--QGDVGYGVYDLYDLGEFFHQKGTIR
SEQ ID NO:116 (1)  AKYSELEGSGGVIMQYFYNDVPEGGIHWDTIRKQIPEWYDAGISAIWIPPSASKGMCGAYSMGYDPYDYLGEFFYQKGTVE

81                                     160
SEQ ID NO:114 (76)  TKYCTKGEQLSAIKLSHSROINVYGDVVINHRKGCADATEDVTAVEVDPADNRNVISGEHRKAWTHFFHPGRGSTYSDFK
SEQ ID NO:128 (79)  TKYCTKTQYLQAIQAASACMQVYADVVFENRKGADSTEWDAVEVNPSPNRNQETSCTYQIQAWTKFDFPGRGNTYSDFK
SEQ ID NO:116 (81)  TRFGSKKEELVNMISTARQYGIKVIADIVINHRAGGDLEWNPYVGDTWTDFSKVASGKYKAHYMDHFPN-----

161                                     240
SEQ ID NO:114 (156)  WEWYHFDGTOWDESRLNRIYKFQG--KAWDMEVSNENQNYDILMYADIYDHPDVAAEIKRWCTWYANELQLDGFRLDA
SEQ ID NO:128 (159)  WRWYHFDGTOWDESRLNRIYKFRCTGKAWDMEVDTEGNYDILMFADLMDHPEVVTTELKNWCTWYVNTTINVDGFRIDA
SEQ ID NO:116 (150)  ----NYSTSDEGTGCGFPDIDHLPFNQYWLWASNES-----YAAIYLRISIGIDAWRFPDY

241                                     320
SEQ ID NO:114 (234)  VKHKIFSEFLRDWVNHVRKTKCKEMETVARYWQNDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQCGGYYDMRKLING--
SEQ ID NO:128 (239)  VKHKIYSFFPDHLTEVRSQTRKNLFAVGEFWSYDVNKLHNYITKTSCTMSLFDAPLHNNFYTASRSGCYFDMRYLLNN--
SEQ ID NO:116 (200)  VKGYCAWVVKDMLQSGWG-----WAVGEYWDTNVDALLNWAYSSG--AKVPDFPLYYKMDFAFNKNIIPALVYAIQNGE

321                                     400
SEQ ID NO:114 (312)  TVVSKHPLKAVTFVDNHDTPQGSLSTVQTFWKPLAYAFILTRGEGYPCVFYGDYMGYTKGDSQ--REIPALKKHIEPIL
SEQ ID NO:128 (317)  TLMKDQPSLAVTLVDNHDTPQGSLQSWVEPWFKPLAYAFILTRQEGYPCVFYGDYIGPKYN-----IPGLSKSIDPLL
SEQ ID NO:116 (272)  TVVSRDPFKAVTFVANEHDTN-----IWNKYPAYAFILTYE--GQPVIFYRDIYEELNKD-----KLNNL---I

401                                     480
SEQ ID NO:114 (390)  KARKQYAYGAQHDFDHDIVGWTRGDSVSSVNSGLAALITDGPCKAKRMVYGRNAGETWHWIDITGNRS--EPVVINSEG
SEQ ID NO:128 (392)  IARRDYAYGTQRDYIDHQDIIIGWTRREGIDSKPNSGLAALITDGPCKGSKMYYGKKHAGKVFYDITGNRS--DTVTINADG
SEQ ID NO:116 (331)  WHEHLAGGSTKILYYDDDELIFMRREGYGRPGL-ITYINLGSWAERWVNVGSKFAGYTIHEYTGNLGGWDRVYQYDG

481                                     560
SEQ ID NO:114 (468)  WEEFVFN-----GGSVSIYVQR-----
SEQ ID NO:128 (470)  WEEFVFN-----GGSVSIWAKTSQVTFVNNATTISQNVYVVGNIPELGNNWTANAIKMTPSSSYTPKATIALP
SEQ ID NO:116 (410)  WVKLTAPPHDPANGYCYGYSWSYAGVG-----

561                                     605
SEQ ID NO:114 (485)  -----
SEQ ID NO:128 (541)  QGKALEFKFIKKDQSGNVVNESIPNRITYTVPFLLTGSYTASWNPV
SEQ ID NO:116 (437)  -----

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**Figure 12: A graph of the pH rate profiles for 2 different amylases.**

